

# Sequencing, Finishing, and Analysis in the Future (SFAF)

La Fonda on the Plaza, Santa Fe, NM — June 1<sup>st</sup> - 3<sup>rd</sup>, 2011

## Call for Abstracts (both talks and posters) Deadline March 30<sup>th</sup>, 2011

Please join us for the 6<sup>th</sup> annual "Sequencing, Finishing and Analysis in the Future" Meeting on Wednesday, June 1<sup>st</sup> through Friday, June 3<sup>rd</sup> in beautiful, historic Santa Fe, New Mexico. The three day SFAF conference will focus on Next Generation Sequencing technologies, applications, and their effect on the rapidly advancing field of Genomics.

### Keynote Speakers:

- John McPherson, Ph.D., Director, Genome Technologies, Ontario Institute for Cancer Research (OICR)
- Karen Nelson, Ph.D., Director, J. Craig Venter Institute (JCVI) Rockville, Maryland Campus
- Folker Meyer, Ph.D., Associate Director, Institute for Genomics and Systems Biology, Argonne Natl. Lab

Areas to be emphasized include, but are not limited to the following:

#### Genome Sequencing:

- New sequencing technologies (454, illumina, SOLiD, Ion Torrent, Pacific Biosciences, etc.)
- Draft sequencing strategies (prokaryotes, eukaryotes, metagenomics, single cell, etc.)
- *De novo* sequencing, re-sequencing, Human seq., RNA seq., metagenomics, etc.

#### Genome Assembly:

- Whole genome assemblers and integration of next generation data
- *De novo* assemblers for short reads, hybrid assemblers
- Recalling and calibrating genome assemblies
- Single cell and metagenomic assemblies

#### Genome Finishing:

- Finishing systems and pipelines (automated, manual, etc.)
- Next generation finishing tools and technologies
- Human Genomics and genome improvement
- Quality standards for new technologies and mixed data sets
- Single cell / cell sorting and metagenomic finishing

#### Genome Analysis:

- Genome annotation and pathway identification tools and pipelines
- Comparative genomics, re-sequencing, SNPs, structural variation
- Large scale data management, cloud computing
- Metagenomic analysis



The conference is being sponsored and hosted by the DOE's Los Alamos National Laboratory and **NO** registration fee is required. Participants need to cover travel costs, hotel and dinner charges. Breakfast, lunch and snacks will be provided. A block of rooms are reserved at the La Fonda at a special conference rate of \$82 per night. **A limited number of extra rooms are available before & after the conference for those that want to stay in the area a little longer (contact Chris Detter for more details).**

Registration is limited to 150; please register soon if you plan to attend. **To register, submit an abstract, or obtain more information as it becomes available please visit our web site, <http://www.lanl.gov/finishinginthefuture/>. Registration will follow the same guidelines as in 2010 (see website for meeting information updates).**

**If you have any questions, or would like further information, please contact Chris Detter at (505)667-1326 or [cdetter@lanl.gov](mailto:cdetter@lanl.gov).**

We look forward to seeing you there!!!

*The 2011 "Sequencing, Finishing and Analysis in the Future" Organizing Committee:*



- \* Chris Detter, Ph.D., JGI- LANL, Genomics Center Director, LANL
- \* Johar Ali, Ph.D., Cancer Genomics Team Leader, OICR
- \* Patrick Chain, Metagenomics Team Leader, LANL
- \* Michael Fitzgerald, Finishing Manager, Broad Institute
- \* Bob Fulton, M.S., Sequence Improvement Group Leader, WashU
- \* Darren Grafham, Sequence, Analysis, Genome Enhancement Coordinator, Sanger Institute
- \* Jessica Hostetler, Genome Finishing and Analysis Manager, JCVI
- \* Alla Lapidus, Ph.D., Director Bioinformatics, IPM, FCCC
- \* Donna Muzny, M.S., Director of Operations, BCM

